RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10 575,626

Source: IFWP

Date Processed by STIC: 3/20/07

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10575,626   CRF Edit Date: 3/20/07
                            Edited by: 7CL

____ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

____ Corrected the SEQ ID NO. Sequence numbers edited were:

_____

____ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

_____

✓ Deleted: ✓___ invalid beginning/end-of-file text ; ___ page numbers

____ Inserted mandatory headings/numeric identifiers, specifically:

_____

____ Moved responses to same line as heading/numeric identifier, specifically:

_____

____ Other:

_____
_____
_____

Revised 09/09/2003

IFWP

RAW SEQUENCE LISTING   DATE: 03/20/2007
PATENT APPLICATION: US/10/575,626   TIME: 17:48:53

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\03202007\J575626.raw

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         3 <110> APPLICANT: Teijin Pharma Limited
W-->     4 <120> TITLE OF INVENTION: New Secretory Protein
W-->     5 <130> FILE REFERENCE: SAP-715-PCT
C-->     6 <140> CURRENT APPLICATION NUMBER: US/10/575,626
C-->     6 <141> CURRENT FILING DATE: 2006-04-13
W-->     6 <160> NUMBER OF SEQ ID: 9
         8 <170> SOFTWARE: PatentIn version 3.1
        10 <210> SEQ ID NO: 1
        11 <211> LENGTH: 978
        12 <212> TYPE: DNA
        13 <213> ORGANISM: human,
        15 <220> FEATURE:
        16 <221> NAME/KEY: CDS
        17 <222> LOCATION: (1)..(951)
        18 <223> OTHER INFORMATION:
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        21 atg gca aag aat cct cca gag aat tgt gaa gac tgt cac att cta aat        48
        22 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn
        23 1               5                   10                  15
        25 gca gaa gct ttt aaa tcc aag aaa ata tgt aaa tca ctt aag att tgt        96
        26 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
        27              20                  25                  30
        29 gga ctg gtg ttt ggt atc ctg gcc cta act cta att gtc ctg ttt tgg       144
        30 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
        31          35                  40                  45
        33 ggg agc aag cac ttc tgg ccg gag gta ccc aaa aaa gcc tat gac atg       192
        34 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
        35      50                  55                  60
        37 gag cac act ttc tac agc aat gga gag aag aag aag att tac atg gaa       240
        38 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
        39 65                  70                  75                  80
        41 att gat cct gtg acc aga act gaa ata ttc aga agc gga aat ggc act       288
        42 Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
        43                  85                  90                  95
        45 gat gaa aca ttg gaa gta cac gac ttt aaa aac gga tac act ggc atc       336
        46 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
        47                  100                 105                 110
        49 tac ttc gtg ggt ctt caa aaa tgt ttt atc aaa act cag att aaa gtg       384
        50 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
        51          115                 120                 125
        53 att cct gaa ttt tct gaa cca gaa gag gaa ata gat gag aat gaa gaa       432
        54 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
        55      130                 135                 140
```

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PATENT APPLICATION: US/10/575,626   TIME: 17:48:53

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\03202007\J575626.raw

```
57 att acc aca act ttc ttt gaa cag tca gtg att tgg gtc cca gca gaa      480
58 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
59 145             150             155             160
61 aag cct att gaa aac cga gat ttt ctt aaa aat tcc aaa att ctg gag      528
62 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
63             165             170             175
65 att tgt gat aac gtg acc atg tat tgg atc aat ccc act cta ata tca      576
66 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser
67             180             185             190
69 gtt tct gag tta caa gac ttt gag gag gag gga gaa gat ctt cac ttt      624
70 Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe
71             195             200             205
73 cct gcc aac gaa aaa aaa ggg att gaa caa aat gaa cag tgg gtg gtc      672
74 Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val
75     210             215             220
77 cct caa gtg aaa gta gag aag acc cgt cac gcc aga caa gca agt gag      720
78 Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
79 225             230             235             240
81 gaa gaa ctt cca ata aat gac tat act gaa aat gga ata gaa ttt gat      768
82 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
83             245             250             255
85 ccc atg ctg gat gag aga ggt tat tgt tgt att tac tgc cgt cga ggc      816
86 Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly
87             260             265             270
89 aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta ggc tac tac cca      864
90 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
91             275             280             285
93 tat cca tac tgc tac caa gga gga cga gtc atc tgt cgt gtc atc atg      912
94 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
95     290             295             300
97 cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg gtc gactacaaag      961
98 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
99 305             310             315
101 acgatgacga caagtga                                                    978
104 <210> SEQ ID NO: 2
105 <211> LENGTH: 317
106 <212> TYPE: PRT
107 <213> ORGANISM: human
109 <400> SEQUENCE: 2
111 Met Ala Lys Asn Pro Pro Glu Asn Cys Glu Asp Cys His Ile Leu Asn
112 1             5               10              15
114 Ala Glu Ala Phe Lys Ser Lys Lys Ile Cys Lys Ser Leu Lys Ile Cys
115             20              25              30
117 Gly Leu Val Phe Gly Ile Leu Ala Leu Thr Leu Ile Val Leu Phe Trp
118             35              40              45
120 Gly Ser Lys His Phe Trp Pro Glu Val Pro Lys Lys Ala Tyr Asp Met
121     50              55              60
123 Glu His Thr Phe Tyr Ser Asn Gly Glu Lys Lys Lys Ile Tyr Met Glu
124 65              70              75              80
```

RAW SEQUENCE LISTING   DATE: 03/20/2007
PATENT APPLICATION: US/10/575,626   TIME: 17:48:53

Input Set : A:\pto.kd.txt
Output Set: N:\CRF4\03202007\J575626.raw

```
126 Ile Asp Pro Val Thr Arg Thr Glu Ile Phe Arg Ser Gly Asn Gly Thr
127              85                  90                  95
129 Asp Glu Thr Leu Glu Val His Asp Phe Lys Asn Gly Tyr Thr Gly Ile
130             100             105             110
132 Tyr Phe Val Gly Leu Gln Lys Cys Phe Ile Lys Thr Gln Ile Lys Val
133         115             120             125
135 Ile Pro Glu Phe Ser Glu Pro Glu Glu Glu Ile Asp Glu Asn Glu Glu
136     130             135             140
138 Ile Thr Thr Thr Phe Phe Glu Gln Ser Val Ile Trp Val Pro Ala Glu
139 145             150             155             160
141 Lys Pro Ile Glu Asn Arg Asp Phe Leu Lys Asn Ser Lys Ile Leu Glu
142             165             170             175
144 Ile Cys Asp Asn Val Thr Met Tyr Trp Ile Asn Pro Thr Leu Ile Ser
145             180             185             190
147 Val Ser Glu Leu Gln Asp Phe Glu Glu Glu Gly Glu Asp Leu His Phe
148         195             200             205
150 Pro Ala Asn Glu Lys Lys Gly Ile Glu Gln Asn Glu Gln Trp Val Val
151     210             215             220
153 Pro Gln Val Lys Val Glu Lys Thr Arg His Ala Arg Gln Ala Ser Glu
154 225             230             235             240
156 Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile Glu Phe Asp
157             245             250             255
159 Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys Arg Arg Gly
160             260             265             270
162 Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly Tyr Tyr Pro
163         275             280             285
165 Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg Val Ile Met
166     290             295             300
168 Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
169 305             310             315
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172 <210> SEQ ID NO: 3
173 <211> LENGTH: 246
174 <212> TYPE: DNA
175 <213> ORGANISM: human
177 <220> FEATURE:
178 <221> NAME/KEY: CDS
179 <222> LOCATION: (1)..(246)
180 <223> OTHER INFORMATION:
W--> 182 <400> 3
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183 caa gca agt gag gaa gaa ctt cca ata aat gac tat act gaa aat gga      48
184 Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly
185 1               5                   10                  15
187 ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt tgt att tac      96
188 Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr
189             20              25                  30
191 tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa cct tta cta     144
192 Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu
193         35              40              45
195 ggc tac tac cca tat cca tac tgc tac caa gga gga cga gtc atc tgt     192
```

```
196 Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
197     50                  55                  60
199 cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg ctg ggg agg      240
200 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg
201 65                  70                  75                  80
203 gtc taa                                                              246
204 Val
208 <210> SEQ ID NO: 4
209 <211> LENGTH: 81
210 <212> TYPE: PRT
211 <213> ORGANISM: human
213 <400> SEQUENCE: 4
215 Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly
216 1                   5                   10                  15
218 Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr
219             20                  25                  30
221 Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu
222         35                  40                  45
224 Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys
225     50                  55                  60
227 Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg
228 65                  70                  75                  80
230 Val
233 <210> SEQ ID NO: 5
234 <211> LENGTH: 303
235 <212> TYPE: DNA
236 <213> ORGANISM: human
238 <220> FEATURE:
239 <221> NAME/KEY: CDS
240 <222> LOCATION: (1)..(303)
241 <223> OTHER INFORMATION:
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W--> 243 <400> 5

```
244 atg cac cat cat cat cat cat gat atc gac tac aaa gac gat gac gac      48
245 Met His His His His His His Asp Ile Asp Tyr Lys Asp Asp Asp Asp
246 1                   5                   10                  15
248 aag tcg cga caa gca agt gag gaa gaa ctt cca ata aat gac tat act      96
249 Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr
250             20                  25                  . 30
252 gaa aat gga ata gaa ttt gat ccc atg ctg gat gag aga ggt tat tgt      144
253 Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys
254             35                  40                  45
256 tgt att tac tgc cgt cga ggc aac cgc tat tgc cgc cgc gtc tgt gaa      192
257 Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu
258     50                  55                  60
260 cct tta cta ggc tac tac cca tat cca tac tgc tac caa gga gga cga      240
261 Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg
262 65                  70                  75                  80
264 gtc atc tgt cgt gtc atc atg cct tgt aac tgg tgg gtg gcc cgc atg      288
265 Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met
```

RAW SEQUENCE LISTING   DATE: 03/20/2007
PATENT APPLICATION: US/10/575,626   TIME: 17:48:53

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\03202007\J575626.raw**

```
266                 85              90                  95
268 ctg ggg agg gtc taa                                         303
269 Leu Gly Arg Val
270                 100
273 <210> SEQ ID NO: 6
274 <211> LENGTH: 100
275 <212> TYPE: PRT
276 <213> ORGANISM: human
278 <400> SEQUENCE: 6
280 Met His His His His His His Asp Ile Asp Tyr Lys Asp Asp Asp Asp
281 1               5                   10                  15
283 Lys Ser Arg Gln Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr
284                 20                  25                  30
286 Glu Asn Gly Ile Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys
287             35                  40                  45
289 Cys Ile Tyr Cys Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu
290     50                  55                  60
292 Pro Leu Leu Gly Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg
293 65                  70                  75                  80
295 Val Ile Cys Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met
296                 85                  90                  95
298 Leu Gly Arg Val
299                 100
302 <210> SEQ ID NO: 7
303 <211> LENGTH: 420
304 <212> TYPE: DNA
305 <213> ORGANISM: human
307 <220> FEATURE:
308 <221> NAME/KEY: CDS
309 <222> LOCATION: (1)..(420)
310 <223> OTHER INFORMATION:
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W--> 312 <400> 7
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313 atg cac cat cat cat cat cat gat atc gac tac aaa gac gat gac gac      48
314 Met His His His His His His Asp Ile Asp Tyr Lys Asp Asp Asp Asp
315 1               5                   10                  15
317 aag tcg cga gaa gtg gta aga aaa att gtt cca act acc aca aaa aga      96
318 Lys Ser Arg Glu Val Val Arg Lys Ile Val Pro Thr Thr Thr Lys Arg
319                 20                  25                  30
321 cca cac agt gga cca cgg agc aac cca ggc gct gga aga ctg aat aat     144
322 Pro His Ser Gly Pro Arg Ser Asn Pro Gly Ala Gly Arg Leu Asn Asn
323             35                  40                  45
325 gaa acc aga ccc agt gtt caa gag gac tca caa gcc ttc aat cct gat     192
326 Glu Thr Arg Pro Ser Val Gln Glu Asp Ser Gln Ala Phe Asn Pro Asp
327     50                  55                  60
329 aat cct tat cat cag cag gaa ggg gaa agc atg aca ttc gac cct aga     240
330 Asn Pro Tyr His Gln Gln Glu Gly Glu Ser Met Thr Phe Asp Pro Arg
331 65                  70                  75                  80
333 ctg gat cac gaa gga atc tgt tgt ata gaa tgt agg cgg agc tac acc     288
334 Leu Asp His Glu Gly Ile Cys Cys Ile Glu Cys Arg Arg Ser Tyr Thr
```

VERIFICATION SUMMARY   DATE: 03/20/2007
PATENT APPLICATION: **US/10/575,626**   TIME: 17:48:54

Input Set : **A:\pto.kd.txt**
Output Set: **N:\CRF4\03202007\J575626.raw**

L:4 M:283 W: Missing Blank Line separator, <120> field identifier
L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
L:182 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:180
L:243 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:241
L:312 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:310

Raw Sequence Listing before editing
(for reference only)

IFWP

RAW SEQUENCE LISTING   DATE: 03/15/2007
PATENT APPLICATION: US/10/575,626   TIME: 11:02:43

Input Set : A:\PTO.SS.txt
Output Set: N:\CRF4\03152007\J575626.raw

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      3 <110> APPLICANT: Teijin Pharma Limited
W-->  4 <120> TITLE OF INVENTION: New Secretory Protein
W-->  5 <130> FILE REFERENCE: SAP-715-PCT
C-->  6 <140> CURRENT APPLICATION NUMBER: US/10/575,626
C-->  6 <141> CURRENT FILING DATE: 2006-04-13
W-->  6 <160> NUMBER OF SEQ ID: 9
      8 <170> SOFTWARE: PatentIn version 3.1
```

Does Not Comply
Corrected Diskette Needed

(PJ.1)

ERRORED SEQUENCES

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    385 <210> SEQ ID NO: 9
    386 <211> LENGTH: 80
    387 <212> TYPE: PRT
    388 <213> ORGANISM: human
    390 <400> SEQUENCE: 9
    392 Ala Ser Glu Glu Glu Leu Pro Ile Asn Asp Tyr Thr Glu Asn Gly Ile
    393 1             5                   10                  15
    395 Glu Phe Asp Pro Met Leu Asp Glu Arg Gly Tyr Cys Cys Ile Tyr Cys
    396             20                  25                  30
    398 Arg Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly
    399             35                  40                  45
    401 Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys Arg
    402         50                  55                  60
    404 Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly Arg Val
    405 65                  70                  75                  80
E--> 408 (14)
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deleted

VERIFICATION SUMMARY DATE: 03/15/2007
PATENT APPLICATION: **US/10/575,626** TIME: 11:02:44

Input Set : **A:\PTO.SS.txt**
Output Set: **N:\CRF4\03152007\J575626.raw**

```
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L:5 M:283 W: Missing Blank Line separator, <130> field identifier
L:6 M:270 C: Current Application Number differs, Replaced Current Application No
L:6 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:6 M:283 W: Missing Blank Line separator, <160> field identifier
L:20 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:18
L:182 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:180
L:243 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:241
L:312 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:310
L:408 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:9
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